

SEQUENCE LISTING

<110> Hyseq, Inc.

<120> A NOVEL EGF MOTIF PROTEIN OBTAINED FROM
A cDNA LIBRARY OF FETAL LIVER-SPLEEN

<130> 20411-720

<140> US 08/968,800

<141> 1997-11-22

<160> 20

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 300

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(300)

<221> misc_feature

<222> (1)...(300)

<223> n = A,T,C or G

<400> 1

ggc tgg aga aga aac agc aag gga gtc tgt gaa gct aca tgc gaa cct 48
Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro
1 5 10 15

gga tgt aag ttt ggt gag tgc gtg gga cca aac aaa tgc aga tgc ttt 96
Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe
20 25 30

cca gga tac acc ggg aaa acc tgc agt caa gat gtg aat gag tgt gga 144
Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly
35 40 45

atg aaa ccc cgg cca tgc caa cac aga tgt gtg aat aca cac gga agc 192
Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser
50 55 60

tac aag tgc ttt tgc ctc agt ggc cac atg ctc atg cca gat gct acg 240
 Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr
 65 70 75 80

tgt gtg aac tcn agg aca tgt gcc atg ata aac tgt cag tat agc tgt 288
 Cys Val Asn Xaa Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
 85 90 95

gaa gac aca gaa 300
 Glu Asp Thr Glu
 100

<210> 2
 <211> 1611
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1506)

<221> misc_feature
 <222> (1)...(1611)
 <223> n = A,T,C or G

<400> 2

ggc tgg aga aga aac agc aag gga gtc tgt gaa gct aca tgc gaa cct 48
 Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro
 1 5 10 15

gga tgt aag ttt ggt gag tgc gtg gga cca aac aaa tgc aga tgc ttt 96
 Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe
 20 25 30

cca gga tac acc ggg aaa acc tgc agt caa gat gtg aat gag tgt gga 144
 Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly
 35 40 45

atg aaa ccc cgg cca tgc caa cac aga tgt gtg aat aca cac gga agc 192
 Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser
 50 55 60

tac aag tgc ttt tgc ctc agt ggc cac atg ctc atg cca gat gct acg 240
 Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr
 65 70 75 80

a
 Cont

tgt gtg aac tcn agg aca tgt gcc atg ata aac tgt cag tat agc tgt Cys Val Asn Xaa Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys 85 90 95	288
gaa gac aca gaa gaa ggg cca cag tgc ctg tgt cca tcc tca gga ctc Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu 100 105 110	336
cgc ctg gcc cca aat gga aga gac tgt cta gat att gat gaa tgt gcc Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala 115 120 125	384
tct ggt aaa gtc atc tgt ccc tac aat cga aga tgt gtg aac aca ttt Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe 130 135 140	432
gga agc tac tac tgc aaa tgt cac att ggt ttc gaa ctg caa tat atc Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu Gln Tyr Ile 145 150 155 160	480
agt gga cga tat gac tgt ata gat ata aat gaa tgt act atg gat agc Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr Met Asp Ser 165 170 175	528
cat acg tgc agc cac cat gcc aat tgc ttc aat acc caa ggg tcc ttc His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe 180 185 190	576
aag tgt aaa tgc aag cag gga tat aaa ggc aat gga ctt cgg tgt tct Lys Cys Lys Cys Gln Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser 195 200 205	624
gct atc cct gaa aat tct gtg aag gaa gtc ctc aga gca cct ggt acc Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala Pro Gly Thr 210 215 220	672
atc aaa gac aga atc aag aag ttg ctt gct cac aaa aac agc atg aaa Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn Ser Met Lys 225 230 235 240	720
aag aag gca aaa att aaa aat gtt acc cca gaa ccc acc agg act cct Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr Arg Thr Pro 245 250 255	768
acc cct aag gtg aac ttg cag ccc ttc aac tat gaa gag ata gtt tcc Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser 260 265 270	816

aga ggc ggg aac tct cat gga ggt aaa aaa ggg aat gaa gag aaa atg Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu Glu Lys Met 275 280 285	864
aaa gag ggg ctt gag gat gag aaa aga gaa gag aaa gcc ctg aag aat Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn 290 295 300	912
gac ata gag gag cga agc ctg cga gga gat gtg ttt ttc cct aag gtg Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe Pro Lys Val 305 310 315 320	960
aat gaa gca ggt gaa ttc ggc ctg att ctg gtc caa agg aaa gcg cta Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg Lys Ala Leu 325 330 335	1008
act tcc aaa ctg gaa cat aaa gat tta aat atc tcg gtt gac tgc agc Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val Asp Cys Ser 340 345 350	1056
ttc aat cat ggg atc tgt gac tgg aaa cag gat aga gaa gat gat ttt Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe 355 360 365	1104
gac tgg aat cct gct gat cga gat aat gct att ggc ttc tat atg gca Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala 370 375 380	1152
gtt ccg gcc ttg gca ggt cac atg aaa gac att ggc cga ttg aaa ctt Val Pro Ala Leu Ala Gly His Met Lys Asp Ile Gly Arg Leu Lys Leu 385 390 395 400	1200
ctc cta cct gac ctg caa ccc caa agc aac ttc tgt ttg ctc ttt gat Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp 405 410 415	1248
tac cgg ctg gcc gga gac aaa gtc ggg aaa ctt cga gtg ttt gtg aaa Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg Val Phe Val Lys 420 425 430	1296
aac agt aac aat gcc ctg gca ttg gag aag acc acg agt gag gat gaa Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu 435 440 445	1344
aag tgg aag aca ggg aaa att cag ttg tat caa gga act gat gct acc Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr 450 455 460	1392

aaa agc atc att ttt gaa gca gaa cgt ggc aag ggc aaa acc ggc gaa 1440
 Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu
 465 470 475 480

atc gca gtg gat ggc gtc ttg ctt gtt tca ggc tta tgt cca gat agc 1488
 Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu Cys Pro Asp Ser
 485 490 495

ctt tta tct gtg gan nnc tgaatggtagtac tatctttata tttgactttg 1536
 Leu Leu Ser Val Xaa Xaa
 500

tatgtcagtt ccctggttt tttgatattt catcatagga cctctggcat tttaaaatta 1596
 ctagctgaaa aattt 1611

<210> 3
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 3
 Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro
 1 5 10 15
 Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe
 20 25 30
 Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly
 35 40 45
 Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser
 50 55 60
 Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr
 65 70 75 80
 Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
 85 90 95
 Glu Asp Thr Glu
 100

<210> 4
 <211> 537
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(537)
 <223> Xaa = Any Amino Acid

<400> 4
 Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro
 1 5 10 15

Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe
 20 25 30
 Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly
 35 40 45
 Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser
 50 55 60
 Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr
 65 70 75 80
 Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
 85 90 95
 Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu
 100 105 110
 Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala
 115 120 125
 Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe
 130 135 140
 Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu Gln Tyr Ile
 145 150 155 160
 Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr Met Asp Ser
 165 170 175
 His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe
 180 185 190
 Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser
 195 200 205
 Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala Pro Gly Thr
 210 215 220
 Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn Ser Met Lys
 225 230 235 240
 Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr Arg Thr Pro
 245 250 255
 Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser
 260 265 270
 Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu Glu Lys Met
 275 280 285
 Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn
 290 295 300
 Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe Pro Lys Val
 305 310 315 320
 Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg Lys Ala Leu
 325 330 335
 Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val Asp Cys Ser
 340 345 350
 Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe
 355 360 365
 Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala
 370 375 380
 Val Pro Ala Leu Ala Gly His Met Lys Asp Ile Gly Arg Leu Lys Leu
 385 390 395 400
 Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp
 405 410 415

Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg Val Phe Val Lys
 420 425 430
 Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu
 435 440 445
 Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr
 450 455 460
 Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu
 465 470 475 480
 Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu Cys Pro Asp Ser
 485 490 495
 Leu Leu Ser Val Asp Asp Xaa Met Val Leu Ser Leu Tyr Leu Thr Leu
 500 505 510
 Tyr Val Ser Ser Leu Val Phe Leu Ile Leu His His Arg Thr Ser Gly
 515 520 525
 Ile Leu Lys Leu Leu Ala Glu Lys Leu
 530 535

<210> 5

<211> 42

<212> PRT

<213> Drosophila Melanogaster

<220>

<221> VARIANT

<222> (1)...(42)

<223> Xaa = Any Amino Acid

<400> 5

Ile Asp Glu Cys Xaa Ser Asn Pro Cys Gln Asn Gly Gly Thr Cys Xaa
 1 5 10 15
 Xaa Xaa Asp Xaa Val Gly Ser Tyr Xaa Cys Xaa Cys Pro Pro Gly Phe
 20 25 30
 Thr Gly Lys Xaa Xaa Xaa Cys Glu Xaa Asn
 35 40

<210> 6

<211> 39

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(39)

<223> Xaa = Any Amino Acid

<400> 6

Xaa Asn Glu Cys Thr Met Xaa Xaa Xaa Cys Gln His Xaa Xaa Xaa Cys
 1 5 10 15
 Val Asn Thr Xaa Gly Ser Tyr Xaa Cys Lys Cys Xaa Ser Gly Xaa Xaa
 20 25 30

Gly Xaa Xaa Leu Xaa Cys Asp
35

<210> 7
<211> 164
<212> PRT
<213> Homo sapiens

<400> 7
Cys Arg Cys Phe Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Val Asn
1 5 10 15
Glu Cys Gly Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr
20 25 30
His Gly Ser Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro
35 40 45
Asp Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
50 55 60
Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu
65 70 75 80
Arg Leu Ala Pro Asn Ile Asp Glu Cys Ala Ser Gly Lys Val Ile Cys
85 90 95
Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe Gly Ser Tyr Tyr Cys Lys
100 105 110
Cys His Ile Gly Phe Glu Leu Gln Tyr Ile Ser Gly Arg Ile Asn Glu
115 120 125
Cys Thr Met Asp Ser His Thr Cys Ser His His Ala Asn Cys Phe Asn
130 135 140
Thr Gln Gly Ser Phe Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly
145 150 155 160
Leu Arg Cys Ser

A
cont
<210> 8
<211> 45
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(45)
<223> Xaa = Any Amino Acid

<400> 8
Val Xaa Glu Cys Xaa Ser Gly Xaa Gln Xaa Xaa Cys Xaa Ser Ser Xaa
1 5 10 15
Xaa Cys Xaa Asn Thr Val Gly Ser Tyr Xaa Cys Arg Cys Arg Pro Gly
20 25 30
Trp Xaa Pro Xaa Pro Gly Xaa Pro Asn Xaa Xaa Xaa Asp
35 40 45

<210> 9
<211> 58
<212> PRT
<213> Mammalian

<220>
<221> VARIANT
<222> (1)...(58)
<223> Xaa = Any Amino Acid

<400> 9
Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His
1 5 10 15
Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn
20 25 30
Cys Val Val Gly Tyr Ile Xaa Xaa Gly Glu Arg Xaa Xaa Cys Gln
35 40 45
Tyr Arg Asp Leu Lys Trp Trp Glu Leu Arg
50 55

<210> 10
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary oligonucleotide primer used in sequence
assembly process

<221> misc_feature
<222> (8)...(8)
<223> n = A, T, C, G, or
1-(2-deoxy-D-ribfuranosyl)-3-nitropyrrole

a
CM
<400> 10
cctttttntt tttgg 15

<210> 11
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary oligonucleotide primer used in sequence
assembly process

<221> misc_feature
<222> (8)...(8)
<223> n = A, T, C, G, or
1-(2-deoxy-D-ribfuranosyl)-3-nitropyrrole

<400> 11
ccaaaaanaaa aaagg

15

<210> 12
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary nucleotide hybridization sequence used
in sequence assembly process

<400> 12
aaaaaaatttt tt

12

<210> 13
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary nucleotide hybridization sequence used
in sequence assembly process

<400> 13
aaaaattttt ta

12

<210> 14
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary nucleotide hybridization sequence used
in sequence assembly process

a
cont
<400> 14
aaaaattttt t

11

<210> 15
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary nucleotide hybridization sequence used
in sequence assembly process

<400> 15

aaaaaatttt tc

12

<210> 16

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<223> Exemplary nucleotide hybridization sequence used
in sequence assembly process

<400> 16

aaaaaatttt tg

12

<210> 17

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<223> Exemplary nucleotide hybridization sequence used
in sequence assembly process

<400> 17

taaaaatttt tt

12

<210> 18

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<223> Exemplary nucleotide hybridization sequence used
in sequence assembly process

<400> 18

caaaaatttt tt

12

<210> 19

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<223> Exemplary nucleotide hybridization sequence used
in sequence assembly process

<400> 19

gaaaaatttt tt

12

<210> 20

<211> 11

<212> DNA

<213> Artificial Sequence

Alt
Cont

<220>

<223> Exemplary nucleotide hybridization sequence used
in sequence assembly process

<400> 20

aaaaaaatttt t

11